ECDC RISK ASSESSMENT

Implication for Europe of the novel influenza A (H1N1) virus

8 May 2009

Source and date of request

ECDC internal decision, 8 May 2009.

Public health issue

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Disease background information

A new influenza A(H1N1) virus was first identified by US CDC on 17 April 2009 in samples from two Californian children. This was reported in the MMWR on 21 April [1]. The basic genetic structure of the virus which was first described in Eurosurveillance on 30 April [2], demonstrated that the virus had many genetic elements from porcine (swine) influenza. The new virus was thus initially called 'swine flu' even though its pig origin later came into question, and it is now clearly evident that it can spread from human to human.

There are now well over 2 000 cases confirmed from at least four continents, with more than 150 from Europe.

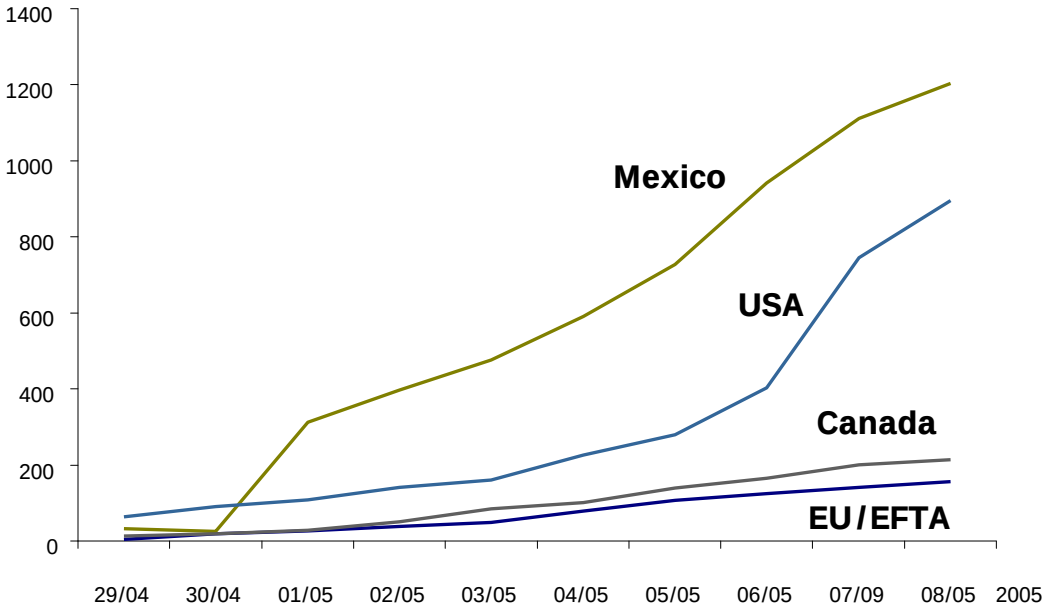
The virus has genetic components from swine influenza (two different swine virus types), avian influenza and human influenza viruses. This is thus a 'quadruple' recombinant virus. Triple recombinant swine influenza viruses with avian, human and swine genes have previously been circulating in pigs in the US, and have been transmitted to humans [3, 4]. There are several recent examples where influenza viruses of animal origin have been transmitted not only from the animal to humans but also from human to human — the most obvious example being the avian H5N1 influenza which has been circulating in Southeast Asia for more than a decade, and which still causes deaths in the region (even if human-to-human transmission has been very limited for this virus).

Stockholm, May 2009

ECDC risk assessment for the EU

The previous threat assessment from 30 April listed a number of unknown parameters needed for proper risk assessment. Many of these are still unknown, and data are still being obtained. However, some answers are beginning to appear.

Cumulative epidemic curve: The daily increase in reported cases has been almost linear in Europe, and very closely follows the development in Canada. Cumulative incidences in Mexico and the US also show linear, although clearly steeper patterns, after initial more rapid increases.



Infectivity: There is now more evidence that the virus transmits in the same way and with the same ease as seasonal influenza, judging from the widespread transmission in the USA. There have already been several estimates of the basic reproductive rate (R_o), which all lie between 1 and 2; the range 1.4 to 1.9 being most probable. This is close to the value observed for seasonal influenza and for previous pandemics. At present in Europe, some 10–15 % of infected returning travellers have spread the disease to other people. There are, however, no certain reports of tertiary transmission in any of the EU/EFTA countries.

Immunity: Laboratory studies are being undertaken and they show some cross-reactivity in sera from older people. Virus of the same subtype, A(H1N1), has been responsible for seasonal flu during several years, but this subtype is quite different. Most of the genes of the novel virus are similar to genes that have developed in pigs — independently of human H1N1 viruses — probably since 1918.

Virulence and risk groups: We still do not know what proportion of infected persons develop the disease and this will have to be assessed in future serological studies. There are no reports of known genetic markers associated with severe disease and even if animal challenges show that the virus does cause disease, the results appear less severe than in the highly pathogenic influenza A(H5N1) for example. To date, the disease seems to have been generally mild in Europe. It should be noted, however, that the majority of cases have been young adults who have returned from travel to the Americas, and who do not constitute a representative cross section of the population.

Spectrum of disease: Its description is in its early stages. The only notable features are preliminary reports that the incubation period for influenza may have a longer tail than observed previously (up to eight days). There are also reports of more gastro-enteric symptoms than common for seasonal influenza. There will probably be many mild cases that will be difficult to differentiate from other respiratory tract infections until serological studies are undertaken.

Case fatality rate: This is unknown at present but there are some severe cases and deaths reported from Mexico and USA. The current reported case fatality rate from Mexico of approximately 4 % is biased, due to more severe cases being diagnosed in that area. The figure for the US of around 1 per 1 000 lies close to what is normally observed for seasonal influenza.

Age distribution: The present peak in the age group 20–29 for the European cases is mainly due to the age of the returning travellers. There are some indications from epidemiology and serology that older people may be less affected perhaps due to some enduring immunological memory of an earlier influenza A(H1N1).

Susceptibility to antivirals: Based on genetic evidence all indications are that the neuraminidase inhibitors oseltamivir and zanamivir will be effective treatment for the novel A(H1N1) influenza virus, but that it is resistant to adamantenes (amantadine and rimantadine). There is some concern that genetic recombination could take place with circulating oseltamivir resistant viruses.

In addition to close surveillance of cases in the EU, ECDC will continue to monitor the situation in Mexico and the US. It is mainly from these two countries that further information will be obtained in order to address the values for the parameters listed above. We will continuously provide information through our website and update this risk assessment as needed. For rapid updates, please see the situation reports published on our website (www.ecdc.europa.eu) every morning.

The current ECDC assessment is that the novel flu virus will continue to spread. Though it seems mild in the USA and in Europe, the overall picture is still unclear as there has not been enough transmission to judge the effects, especially in those population groups more at risk. Also, pandemic viruses are unpredictable and can change their characteristics as they evolve. Even pandemics usually slow down in summer, only to pick up in autumn, and the virus may then come back, perhaps in a more aggressive form than in 1919.

References

1. www.cdc.gov/mmwr/preview/mmwrhtml/mm5815a5.htm — Vol 58, No 15;400

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3. Olsen, C.W., et al.Triple reassortant H3N2 influenza A viruses, Canada, 2005. Emerg Infect Dis, 2006. 12(7): p. 1132-5.

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